```
                .         .         .         .         .         .
  1 ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG   60
  1 M  S  S  R  I  A  R  A  L  A  L  V  V  T  L  L  H  L  T  R    20

                .         .         .         .         .         .
 61 CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG   120
 21 L  A  L  S  T  C  P  A  A  C  H  C  P  L  E  A  P  K  C  A    40

                .         .         .         .         .         .
121 CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC   180
 41 P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L    60

                .         .         .         .         .         .
181 AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC   240
 61 N  E  D  C  S  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F    80

                .         .         .         .         .         .
241 GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT   300
 81 G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C    100

                .         .         .         .         .         .
301 GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG   360
101 E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q    120

                .         .         .         .         .         .
361 TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC   420
121 C  T  C  I  D  G  A  V  G  C  I  P  L  C  P  Q  E  L  S  L    140

                .         .         .         .         .         .
421 CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG   480
141 P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E  E    160

                .         .         .         .         .         .
481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC   540
161 W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L  G    180

                .         .         .         .         .         .
541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA   600
181 K  E  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I  A    200

                .         .         .         .         .         .
601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA   660
201 V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I  L    220
```

FIG.1A

```
                .         .         .         .         .         .
661  TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA  720
221  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  W  S  Q  C  S   240

                .         .         .         .         .         .
721  AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT  780
241  K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R  L   260

                .         .         .         .         .         .
781  GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG  840
261  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S  L   280

                .         .         .         .         .         .
841  AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC  900
281  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T  Y   300

                .         .         .         .         .         .
901  GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC  960
301  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D  G   320

                .         .         .         .         .         .
961  CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG  1020
321  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  R  C  E  D  G   340

                .         .         .         .         .         .
1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG  1080
341  E  T  F  S  K  N  V  M  M  I  Q  S  C  K  C  N  Y  N  C  P   360

                .         .         .         .         .         .
1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG  1140
361  H  A  N  E  A  A  F  P  F  Y  R  L  F  N  D  I  H  K  F  R   380
1141 GACTAA  1146
381  D  *    382
```

FIG. 1B

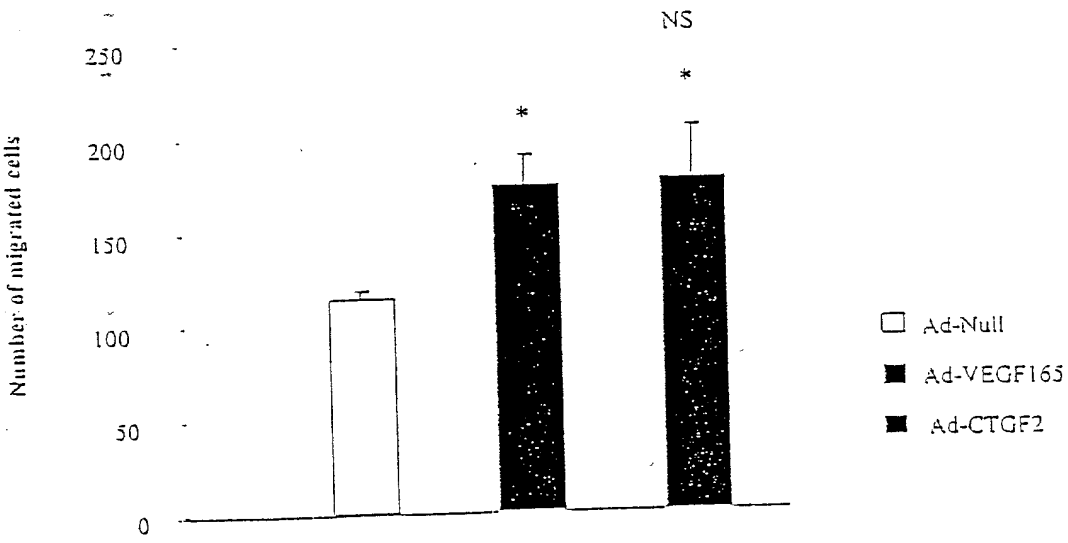
Number of migrated cells
250
200
150
100
50
0
*
NS
*
Ad-Null
Ad-VEGF165
Ad-CTGF2

FIG. 2

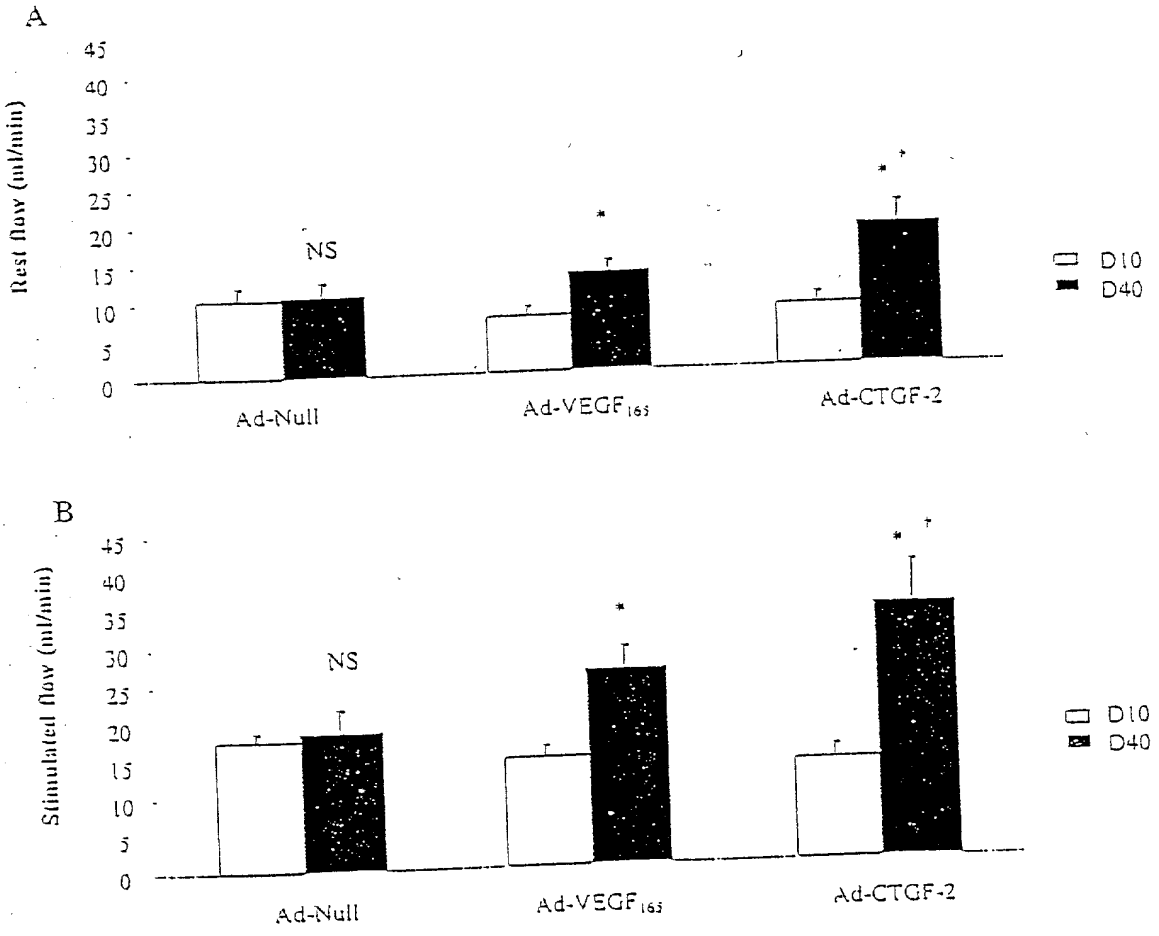
A
Rest flow (ml/min)
45
40
35
30
25
20
15
10
5
0
NS
*
*
Ad-Null
Ad-VEGF165
Ad-CTGF-2
D10
D40
B
Stimulated flow (ml/min)
45
40
35
30
25
20
15
10
5
0
NS
*
*
Ad-Null
Ad-VEGF165
Ad-CTGF-2
D10
D40

FIG. 3

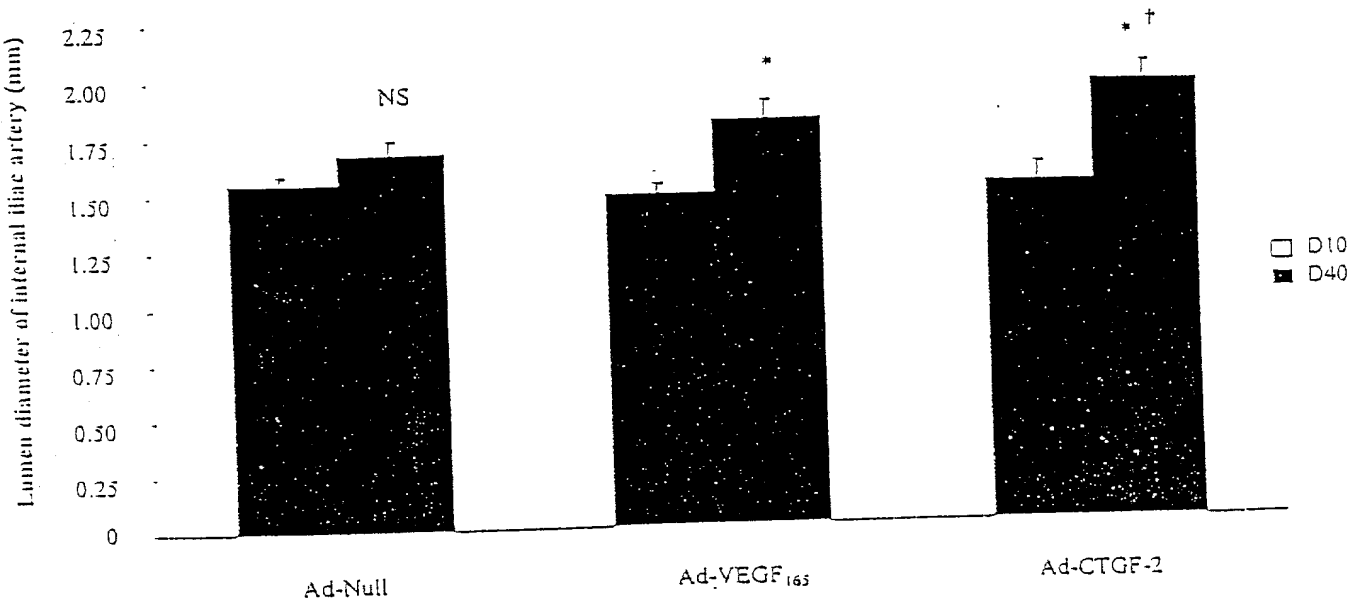
Lumen diameter of internal iliac artery (mm)
2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0
NS
*
* †
D10
D40
Ad-Null
Ad-VEGF165
Ad-CTGF-2

FIG. 4

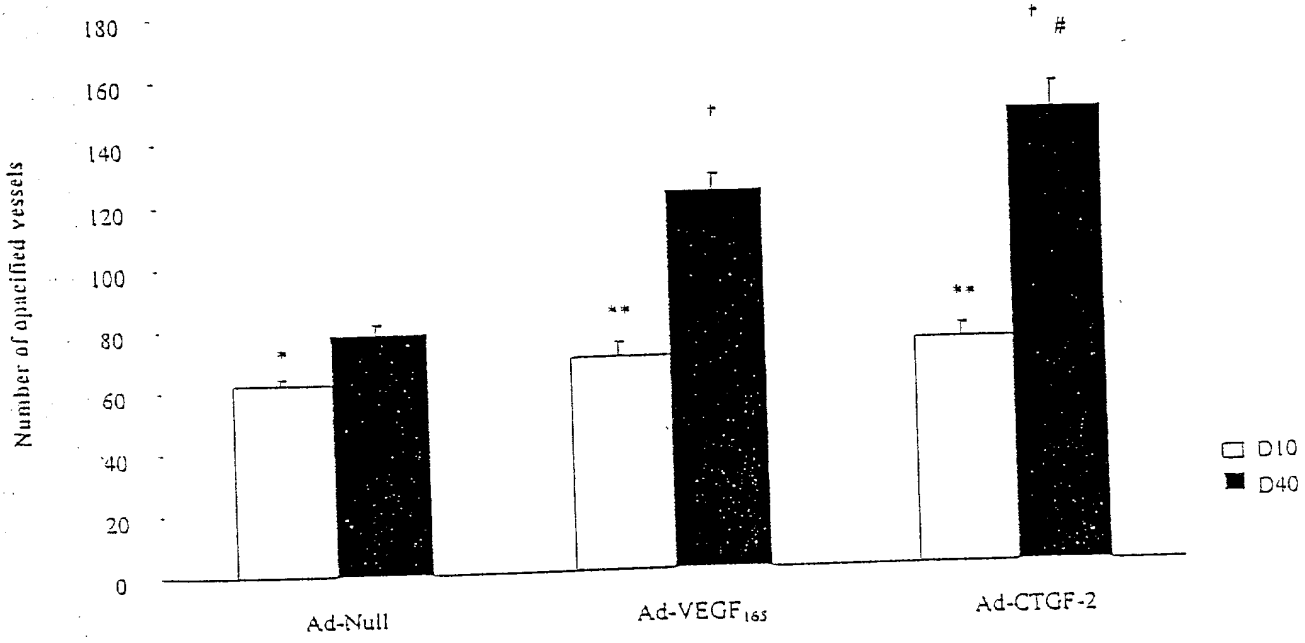
Number of opacified vessels
180
160
140
120
100
80
60
40
20
0
*
**
†
**
†
#
Ad-Null
Ad-VEGF165
Ad-CTGF-2
D10
D40

FIG. 5

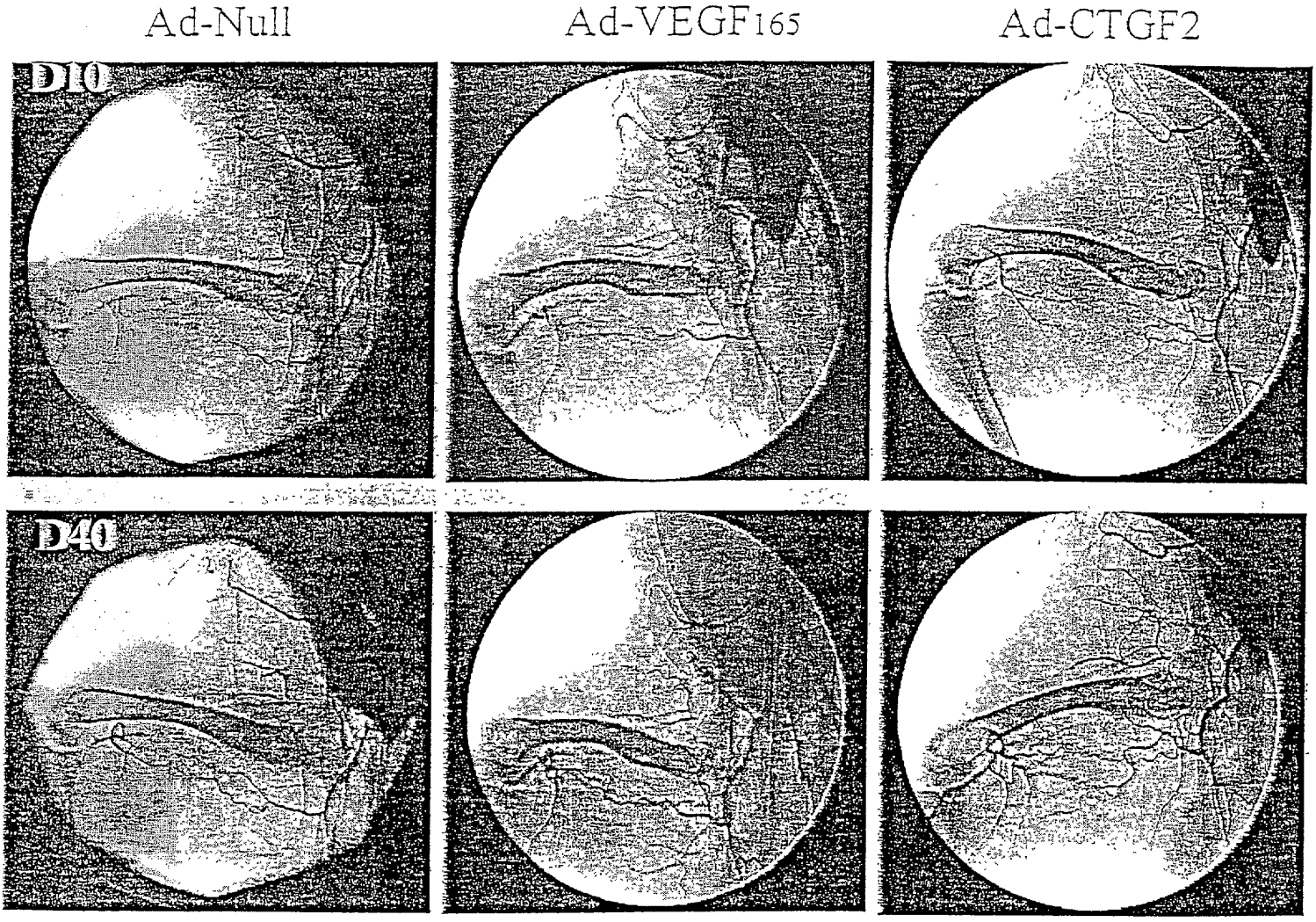

FIG. 6

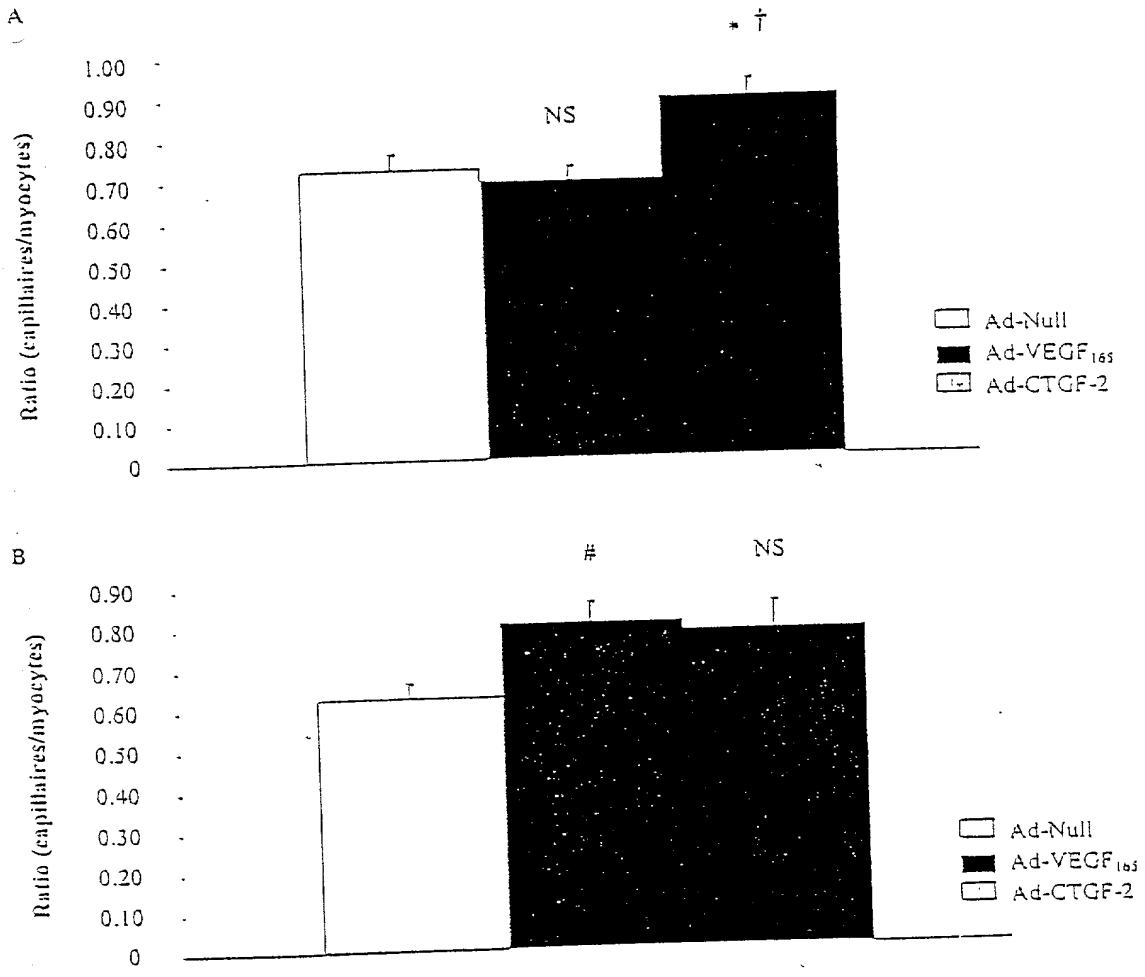
A
* †
NS
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
Ratio (capillaires/myocytes)
Ad-Null
Ad-VEGF165
Ad-CTGF-2
B
#
NS
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
Ratio (capillaires/myocytes)
Ad-Null
Ad-VEGF165
Ad-CTGF-2

FIG. 7

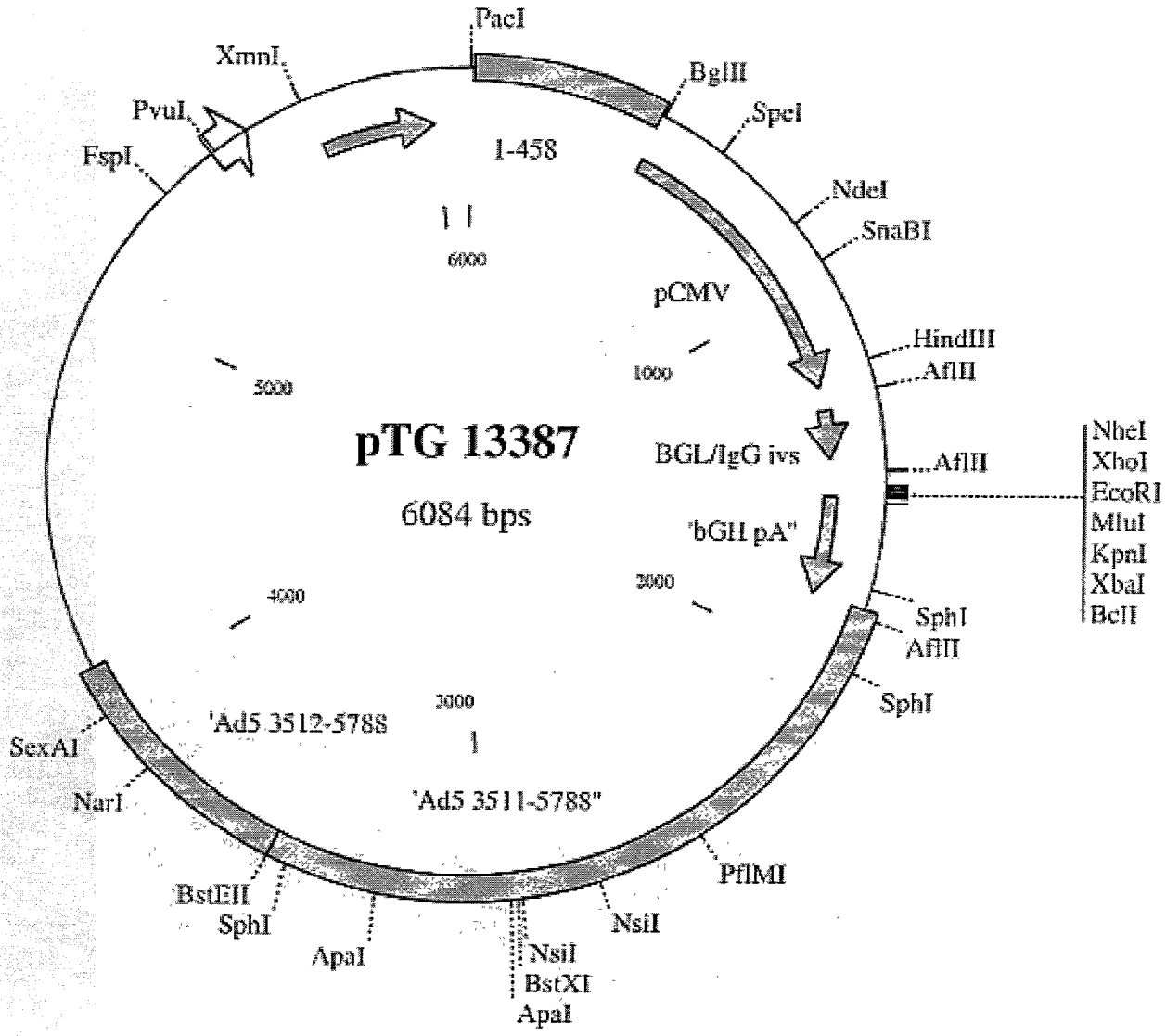
PacI
XmnI
BglII
PvuI
SpeI
FspI
1-458
NdeI
SnaBI
6000
pCMV
HindIII
AflII
5000
1000
pTG 13387
BGL/IgG ivs
AflII
NheI
XhoI
EcoRI
MfuI
KpnI
XbaI
BclI
6084 bps
'bGH pA"
4000
2000
SphI
AflII
SphI
3000
'Ad5 3512-5788
SexAI
'Ad5 3511-5788"
NarI
PflMI
BstEII
SphI
NsiI
ApaI
NsiI
BstXI
ApaI

FIG. 8

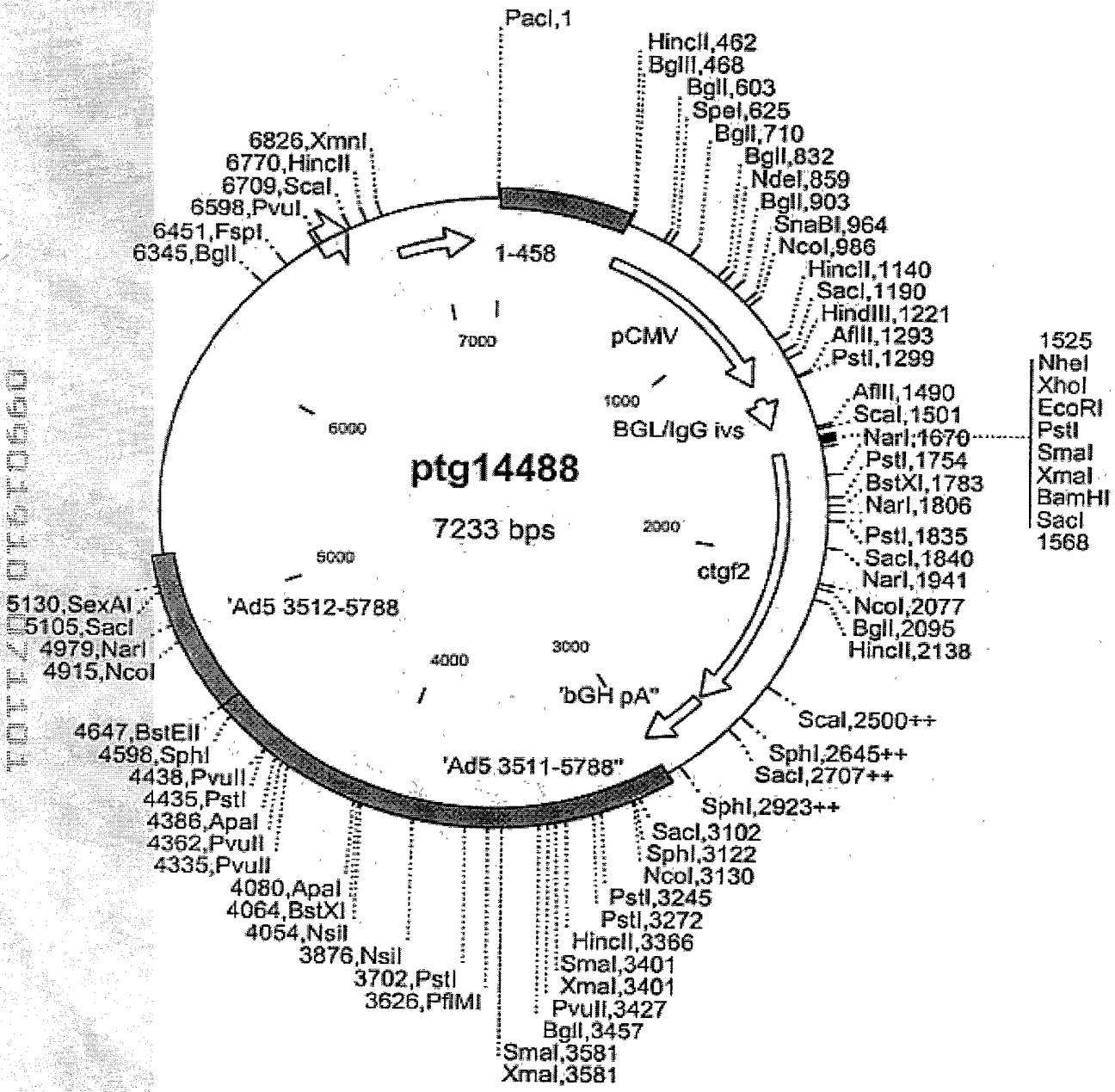
ptg14488
7233 bps
pCMV
BGL/IgG ivs
ctgf2
'bGH pA"
'Ad5 3511-5788"
'Ad5 3512-5788
1-458
1000
2000
3000
4000
5000
6000
7000
PacI,1
HincII,462
BglII,468
BglI,603
SpeI,625
BglI,710
BglI,832
NdeI,859
BglI,903
SnaBI,964
NcoI,986
HincII,1140
SacI,1190
HindIII,1221
AflII,1293
PstI,1299
AflII,1490
ScaI,1501
NarI,1670
PstI,1754
BstXI,1783
NarI,1806
PstI,1835
SacI,1840
NarI,1941
NcoI,2077
BglI,2095
HincII,2138
ScaI,2500++
SphI,2645++
SacI,2707++
SphI,2923++
SacI,3102
SphI,3122
NcoI,3130
PstI,3245
PstI,3272
HincII,3366
SmaI,3401
XmaI,3401
PvuII,3427
BglI,3457
SmaI,3581
XmaI,3581
3626,PflMI
3702,PstI
3876,NsiI
4054,NsiI
4064,BstXI
4080,ApaI
4335,PvuII
4362,PvuII
4386,ApaI
4435,PstI
4438,PvuII
4598,SphI
4647,BstEII
4915,NcoI
4979,NarI
5105,SacI
5130,SexAI
6345,BglI
6451,FspI
6598,PvuI
6709,ScaI
6770,HincII
6826,XmnI
1525
NheI
XhoI
EcoRI
PstI
SmaI
XmaI
BamHI
SacI
1568

FIG. 9

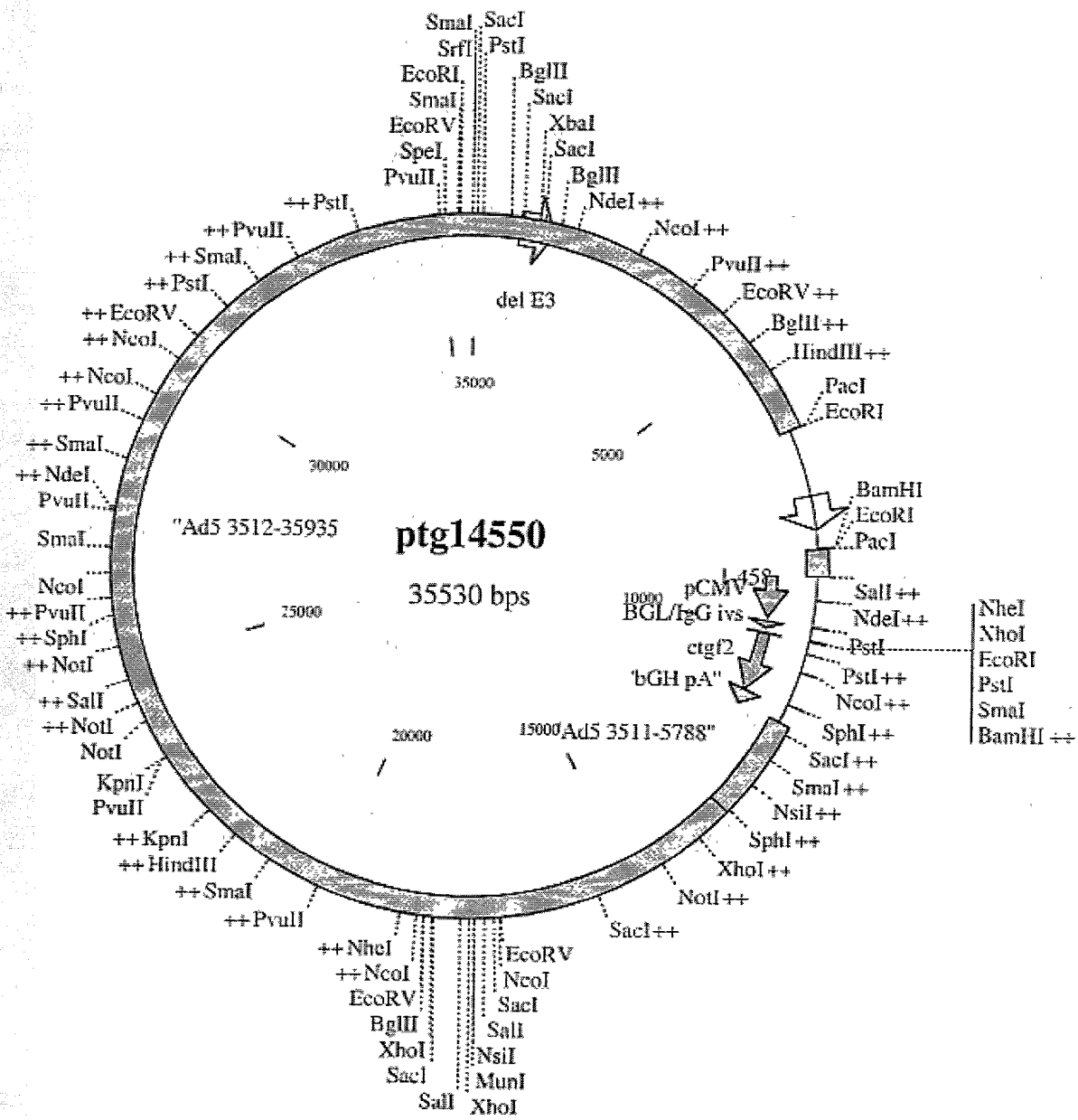
ptg14550
35530 bps
"Ad5 3512-35935
"Ad5 3511-5788"
del E3
pCMV
BGL/IgG ivs
ctgf2
'bGH pA"
5000
10000
15000
20000
25000
30000
35000
SmaI
SacI
SrfI
PstI
EcoRI
BglII
SmaI
SacI
EcoRV
XbaI
SpeI
SacI
PvuII
BglII
++PstI
NdeI++
++PvuII
NcoI++
++SmaI
PvuII++
++PstI
EcoRV++
++EcoRV
BglII++
++NcoI
HindIII++
++NcoI
PacI
++PvuII
EcoRI
++SmaI
++NdeI
BamHI
PvuII
EcoRI
SmaI
PacI
NcoI
SalI++
++PvuII
NdeI++
++SphI
PstI
++NotI
PstI++
++SalI
NcoI++
++NotI
SphI++
NotI
SacI++
KpnI
SmaI++
PvuII
NsiI++
++KpnI
SphI++
++HindIII
XhoI++
++SmaI
NotI++
++PvuII
SacI++
++NheI
++NcoI
EcoRV
NcoI
EcoRV
SacI
BglII
SalI
XhoI
NsiI
SacI
MunI
SalI
XhoI
NheI
XhoI
EcoRI
PstI
SmaI
BamHI ++

FIG. 10

FIG. 11A

MATCH WITH FIG. 11B

FIG. 11B

MATCH WITH FIG. 11A

```
GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L

GGCAAGGGGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G  K  G  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATC
A  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  V  S  Q  C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S  K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R

CTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGC
L  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACT
L  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T
```

MATCH WITH FIG. 11C

MATCH WITH FIG. 11B

FIG. 11C

```
TACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGAC
Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCCCTGCGAAGAT
G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAATGA
P  H  A  N  E  A  A  F  P  F  Y  R  L  F  Q  *
```